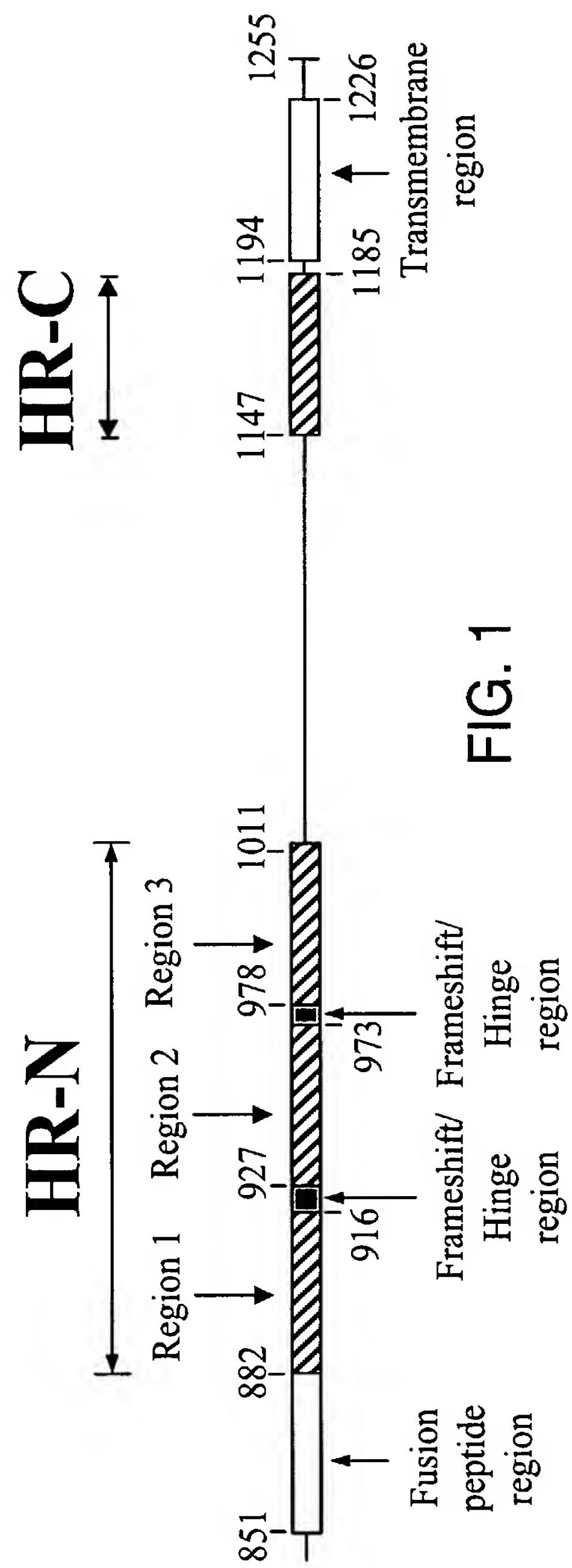
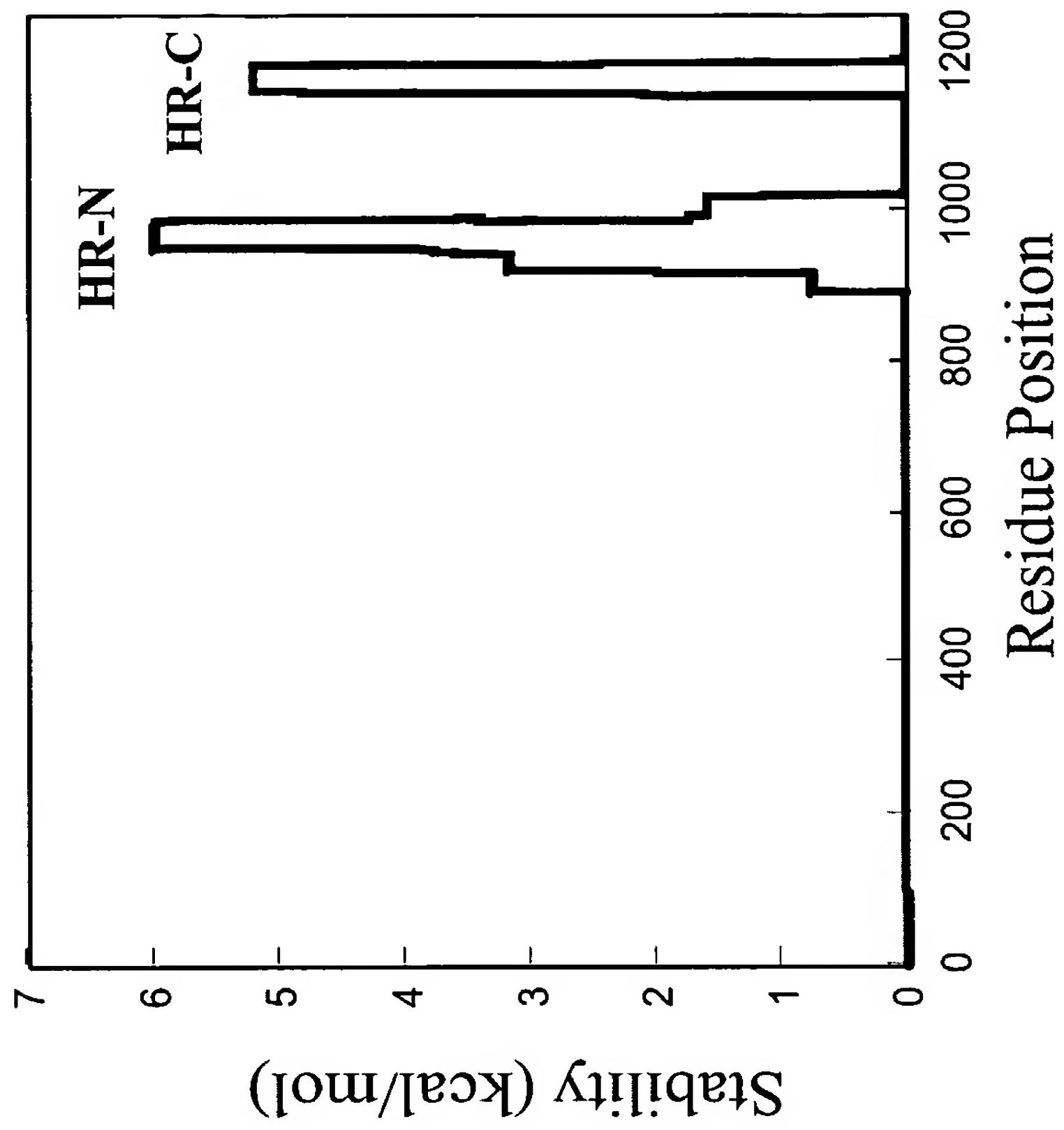
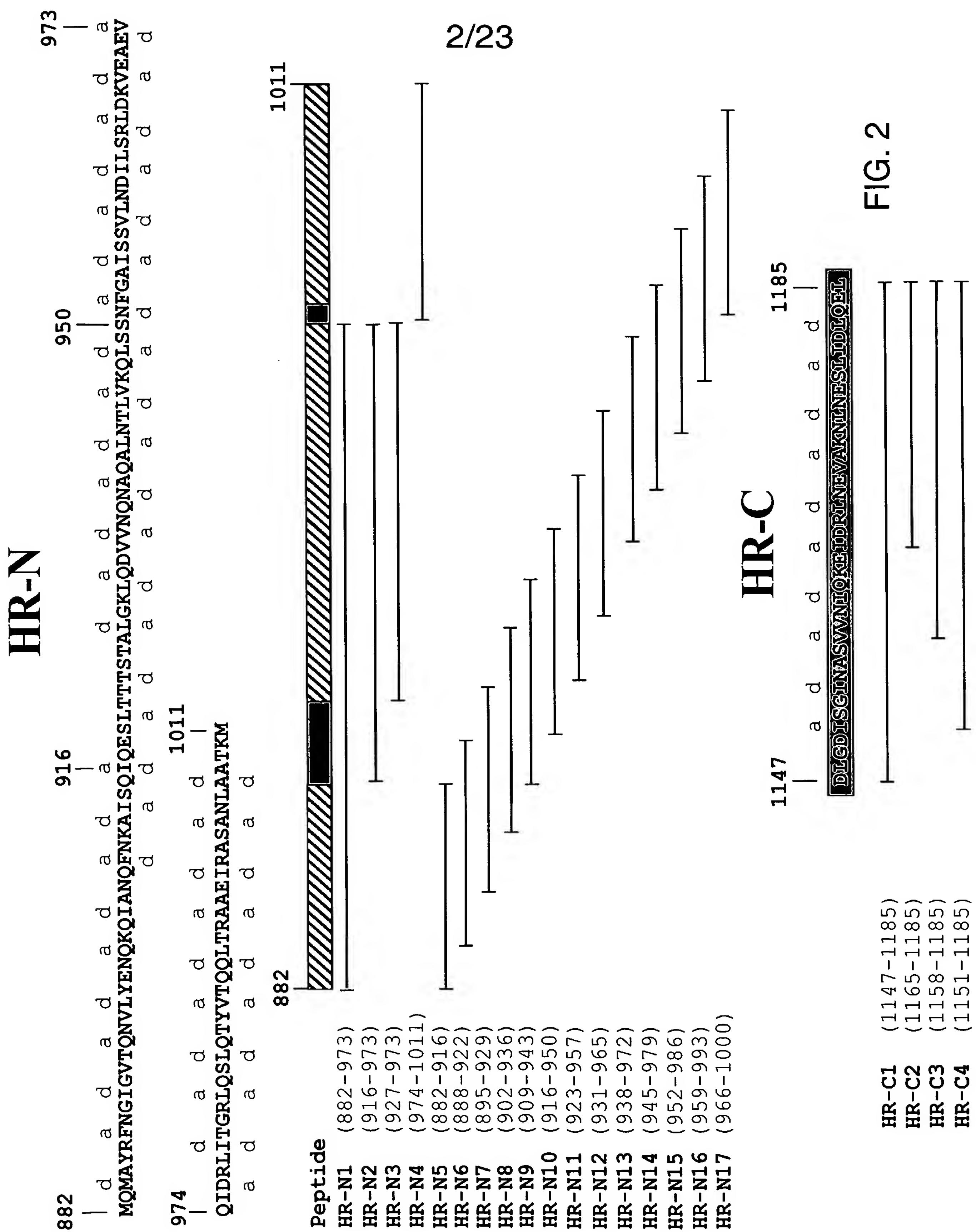


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**FIG. 1**



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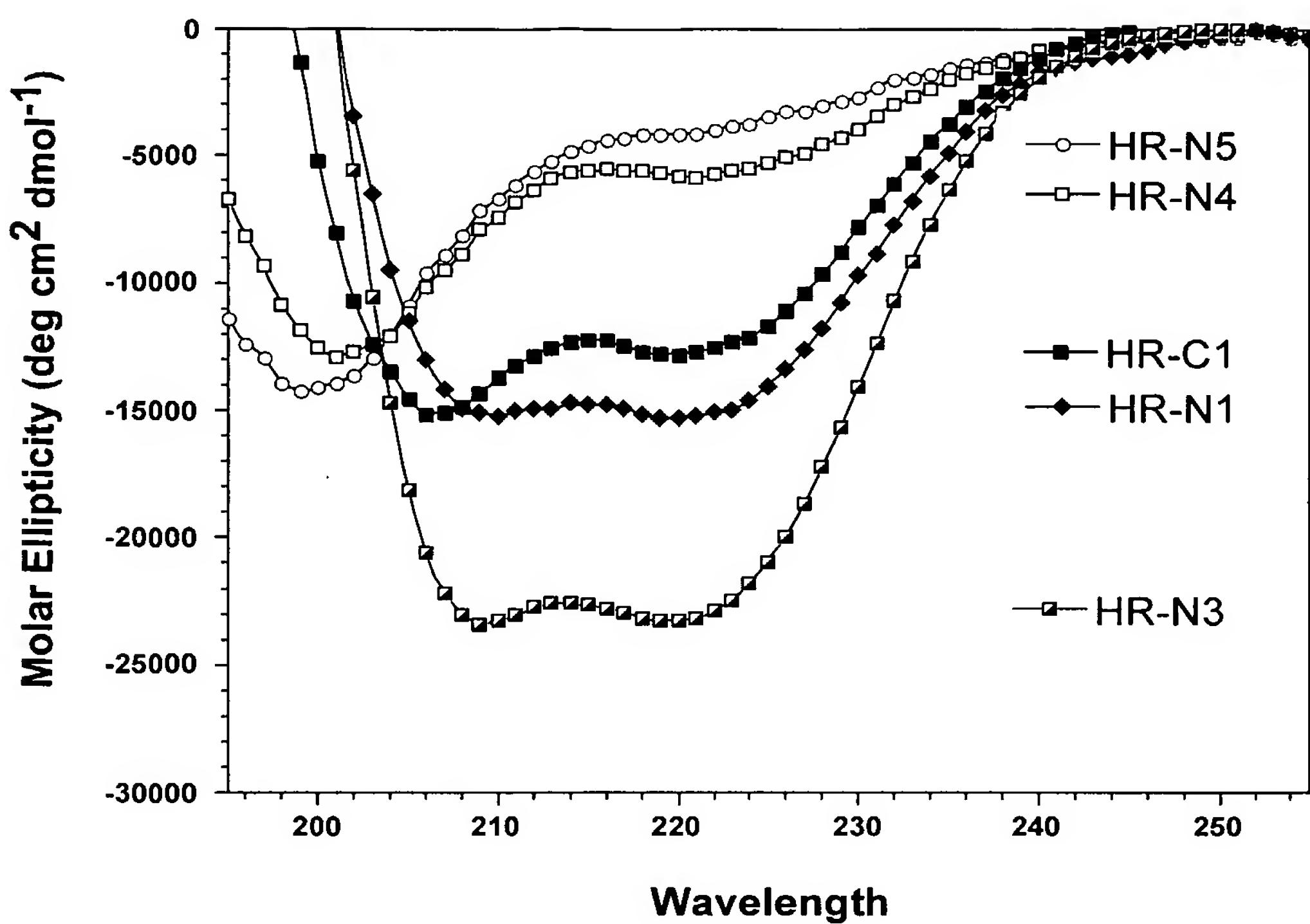
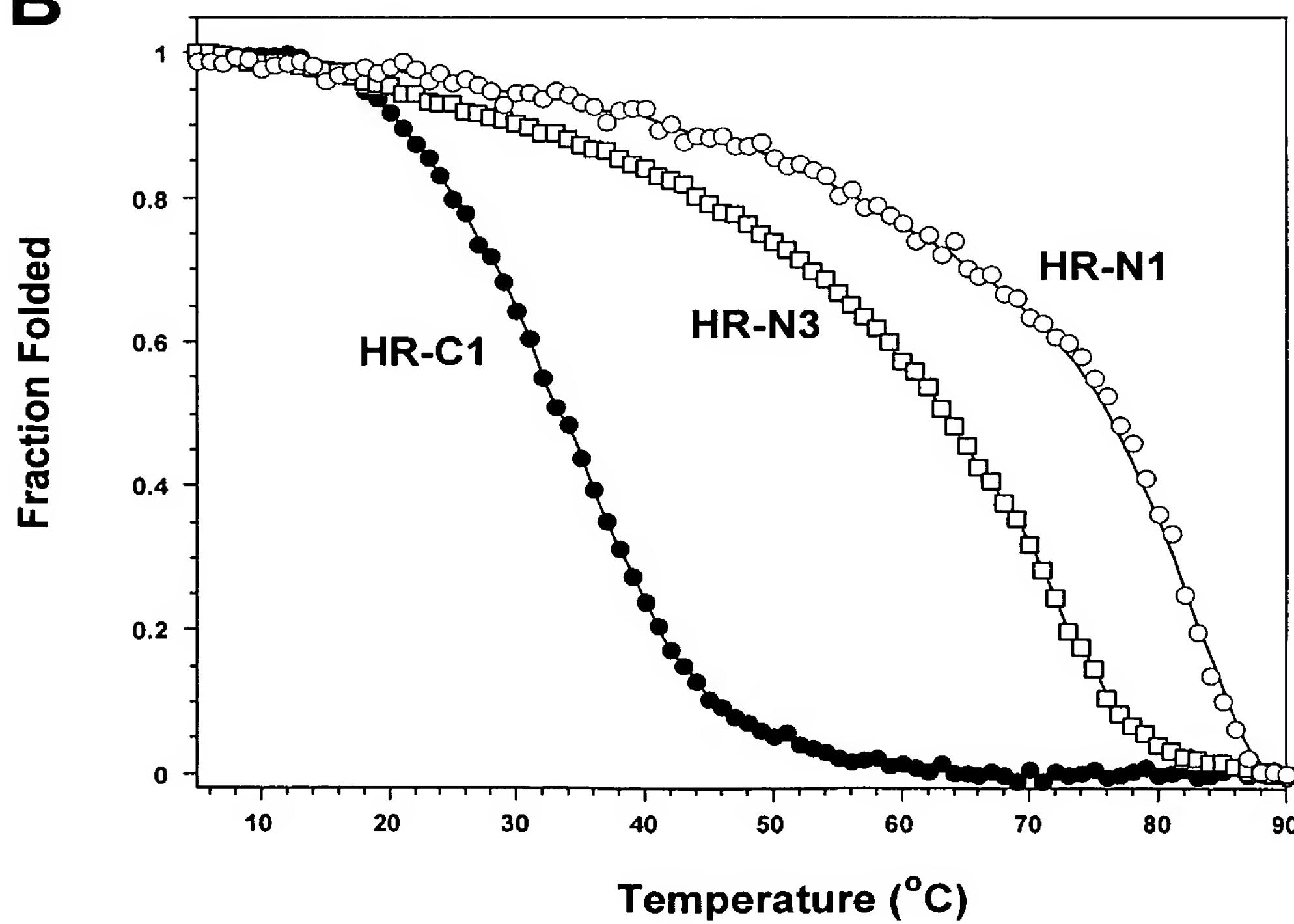
**A****B**

FIG. 3

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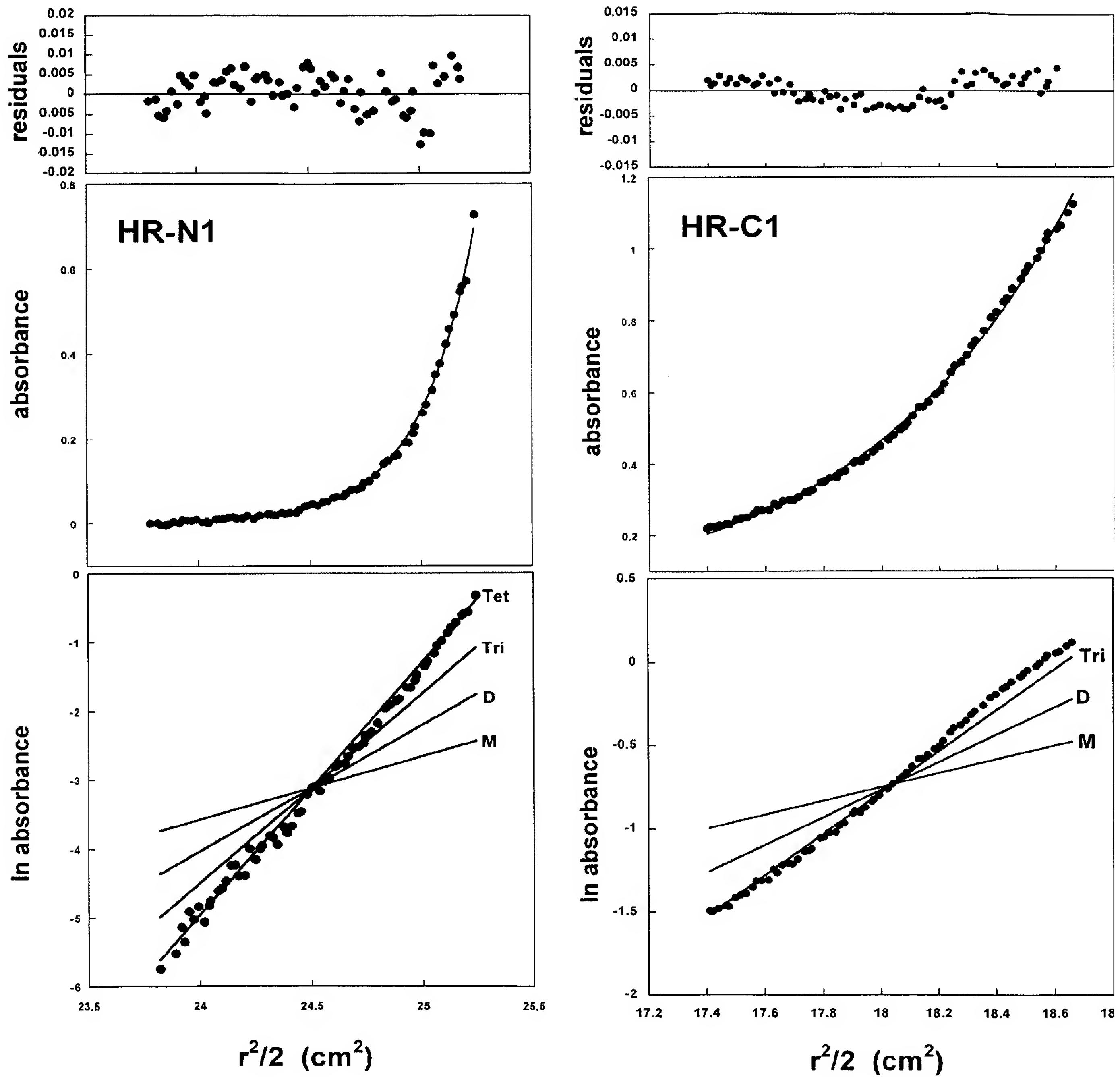
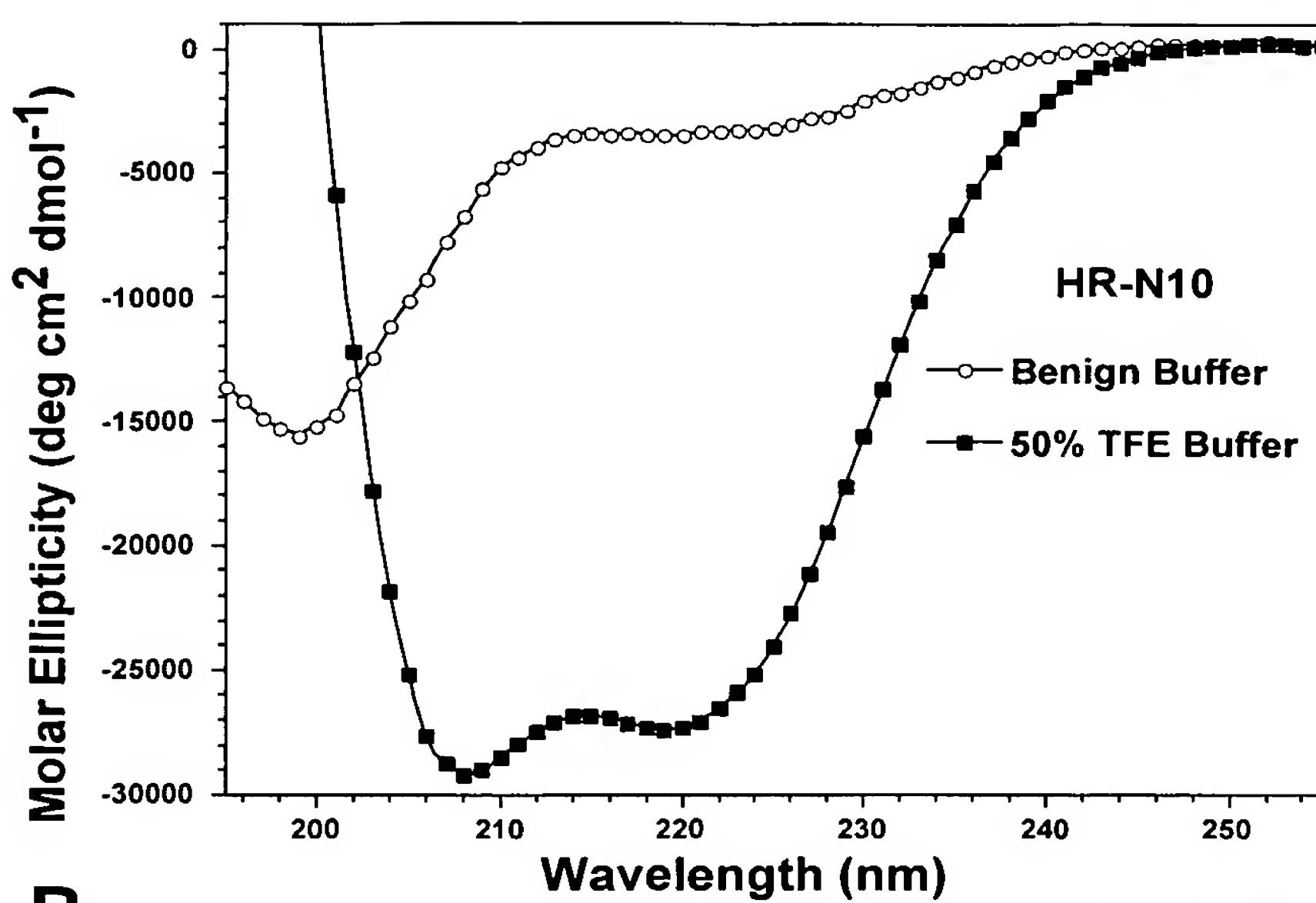
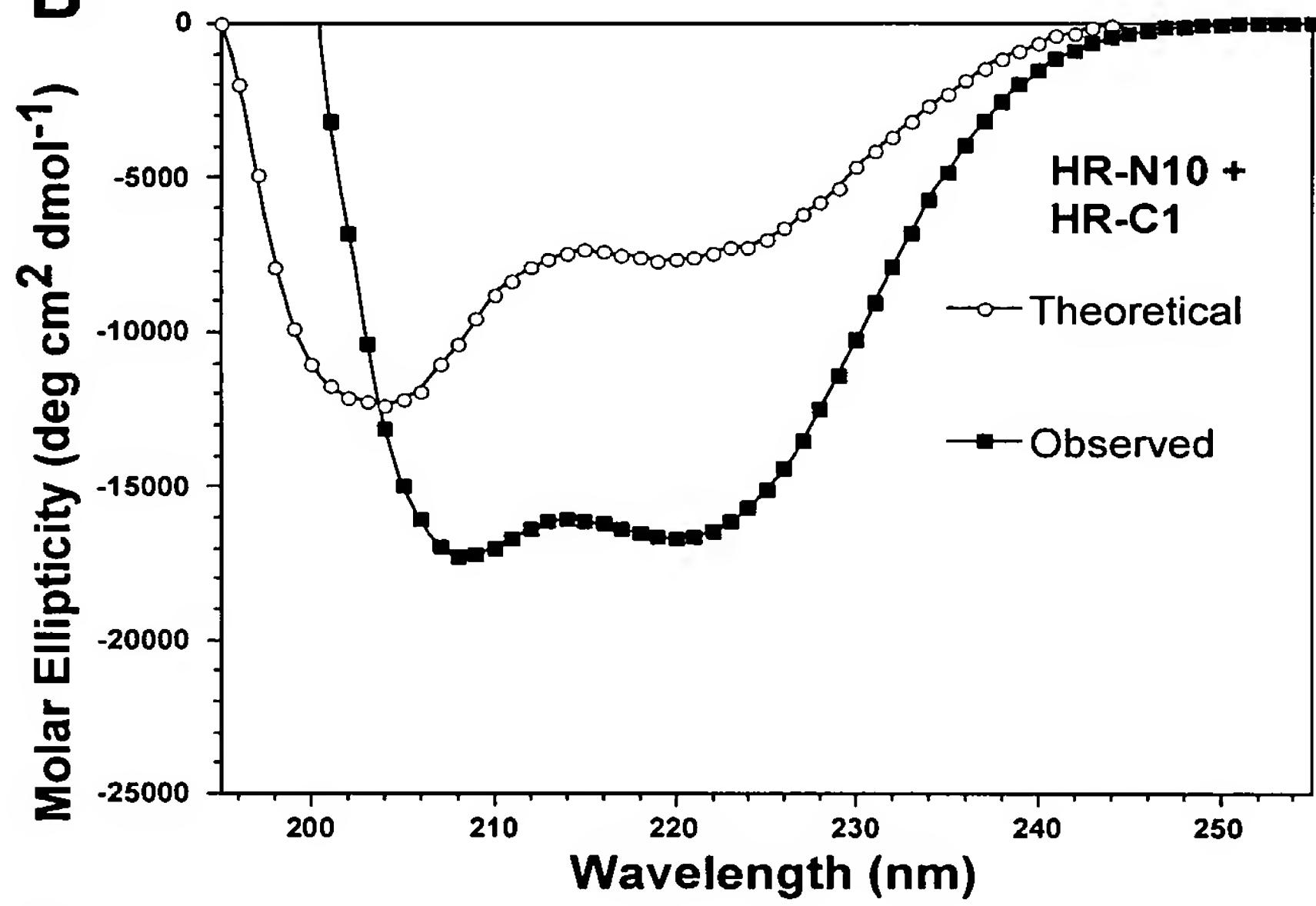
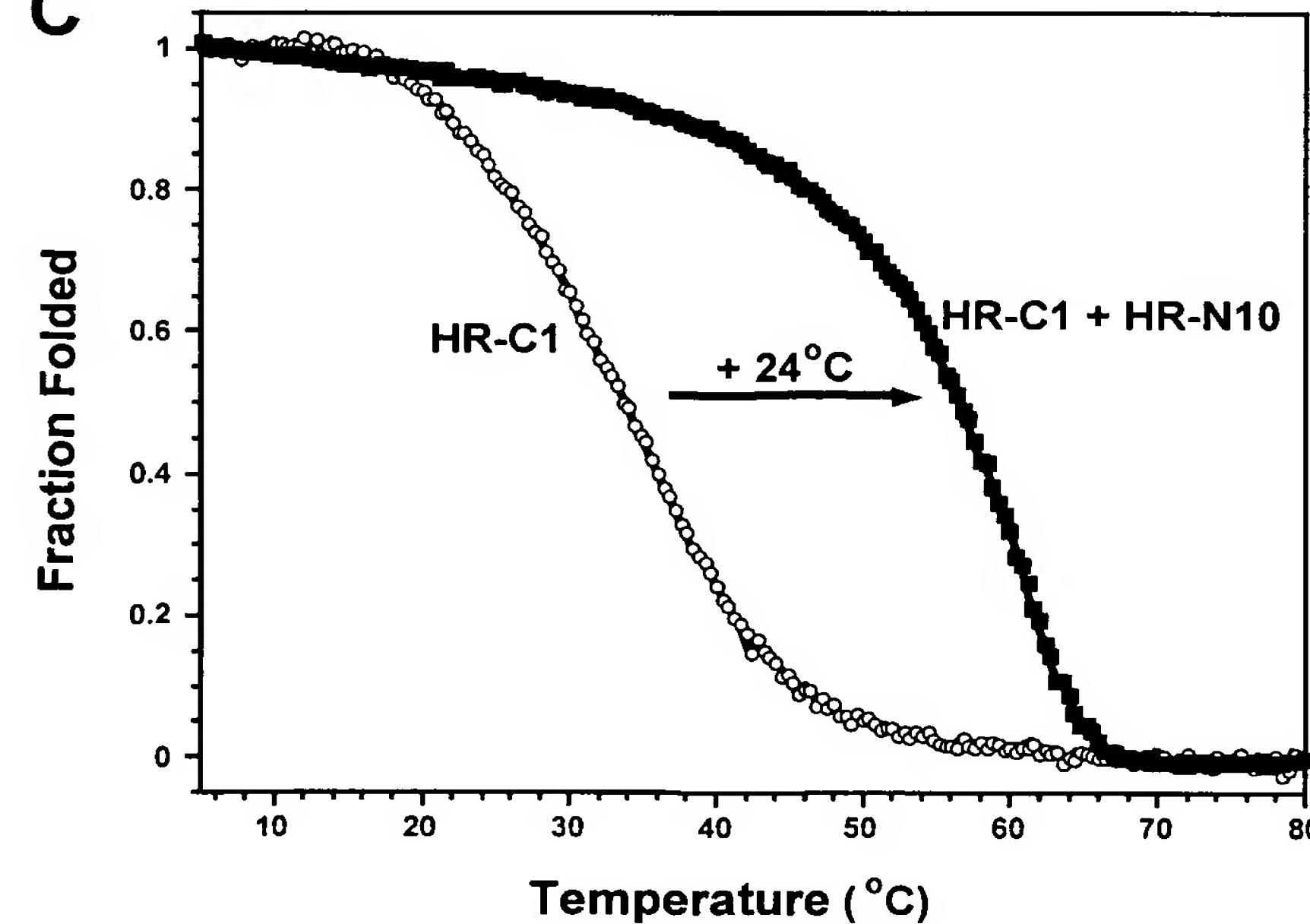


FIG. 4

**A**

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**B****C****FIG. 5**

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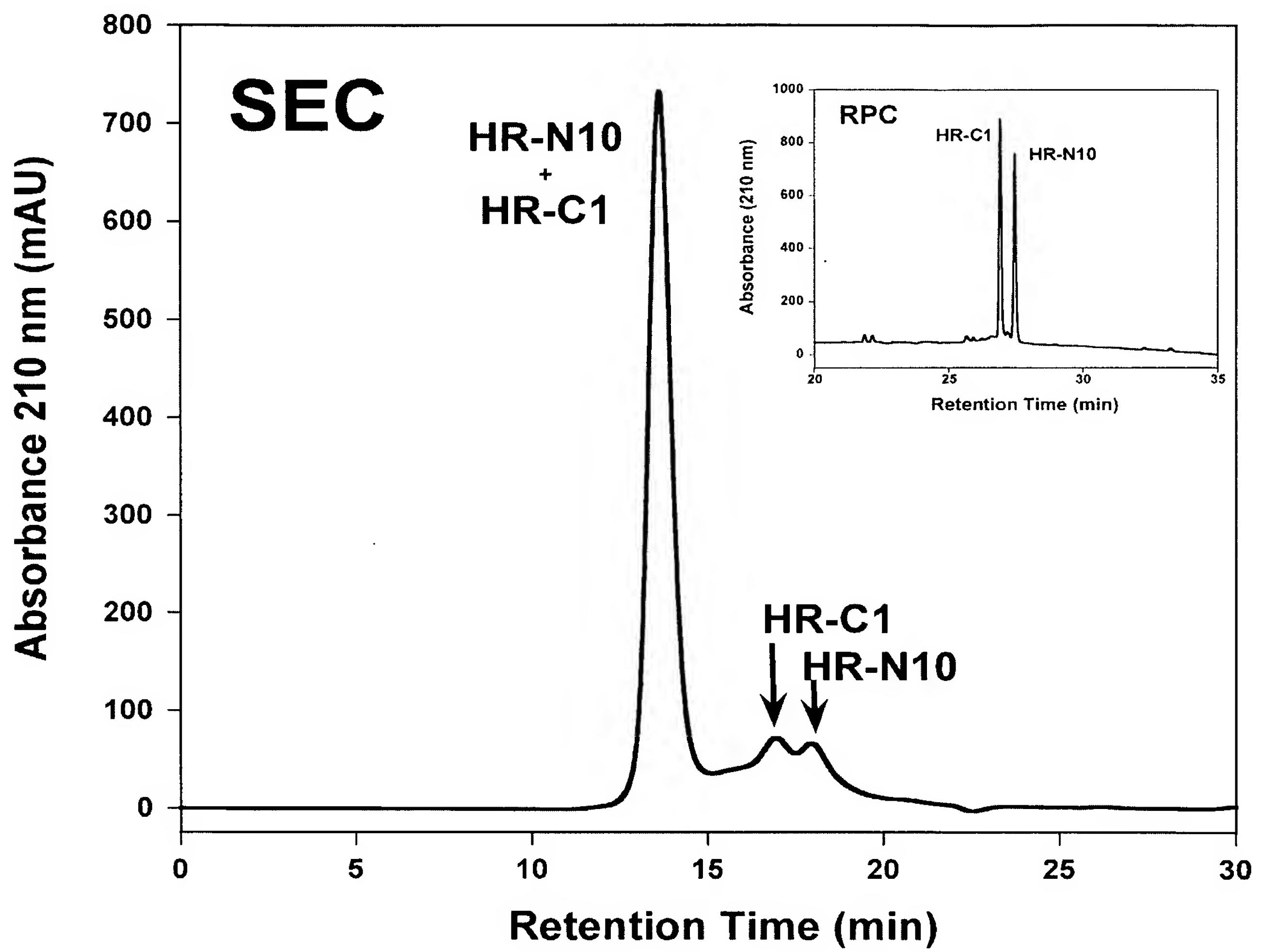


FIG. 6

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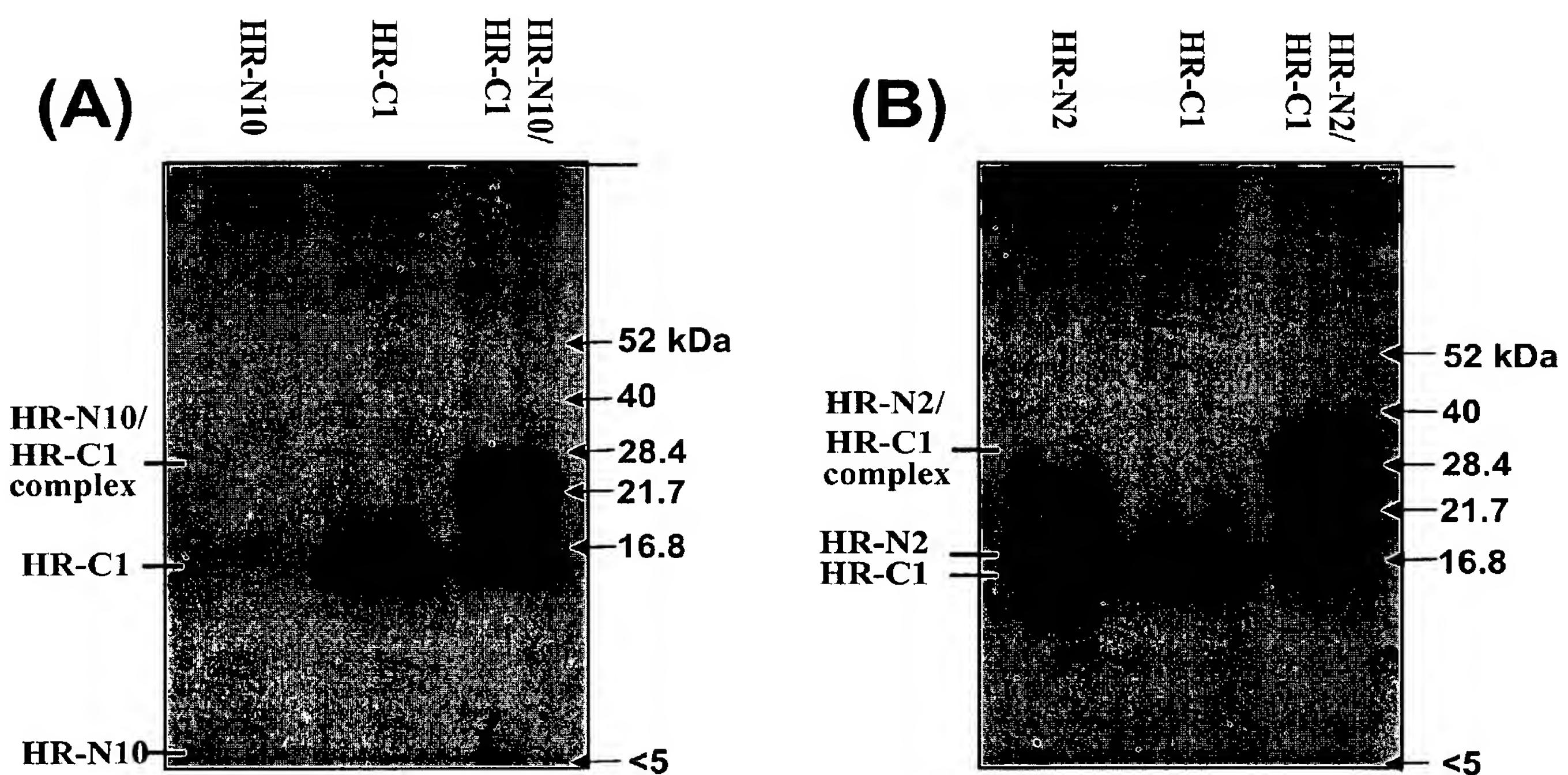


FIG. 7

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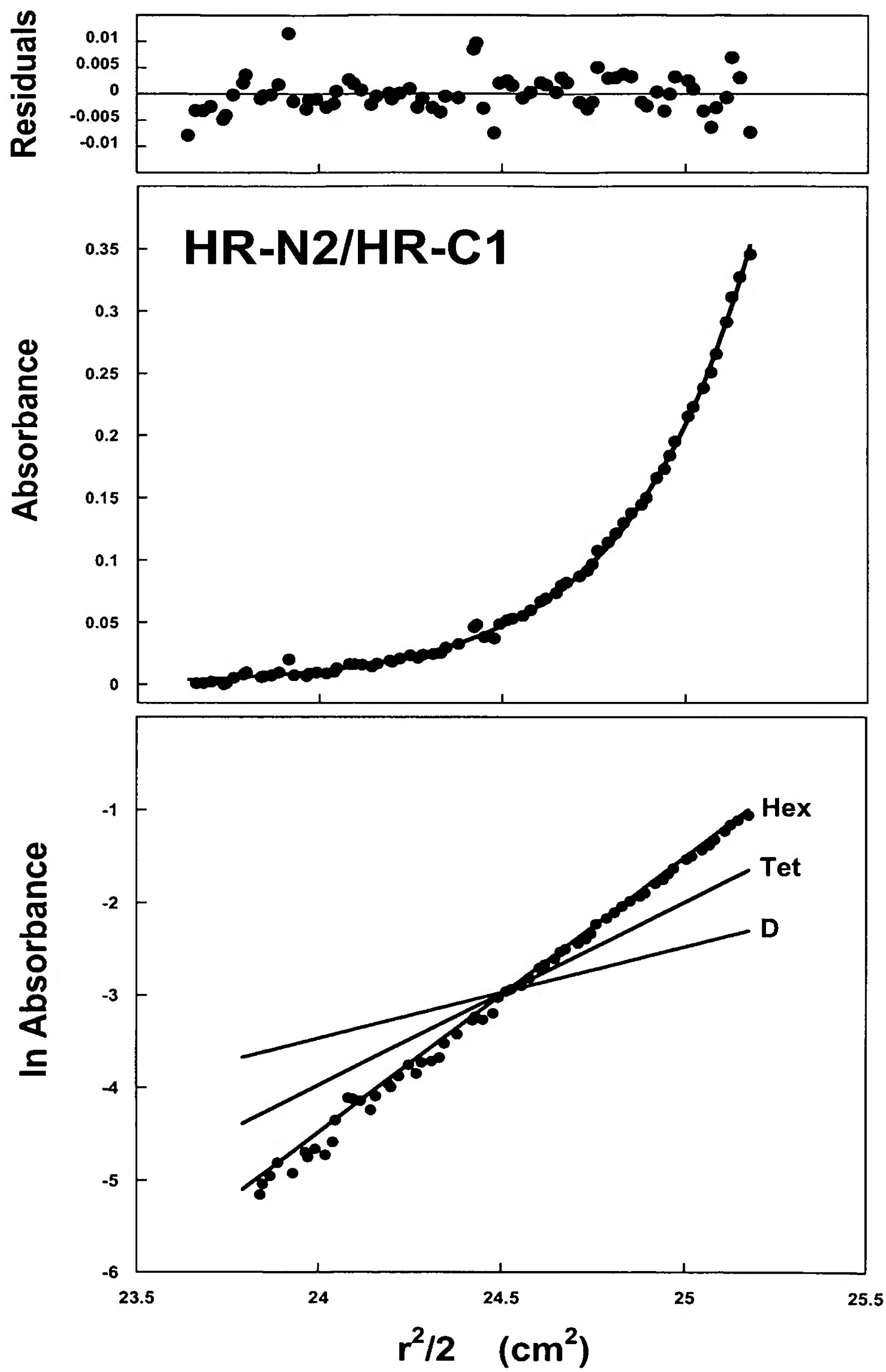


FIG. 8

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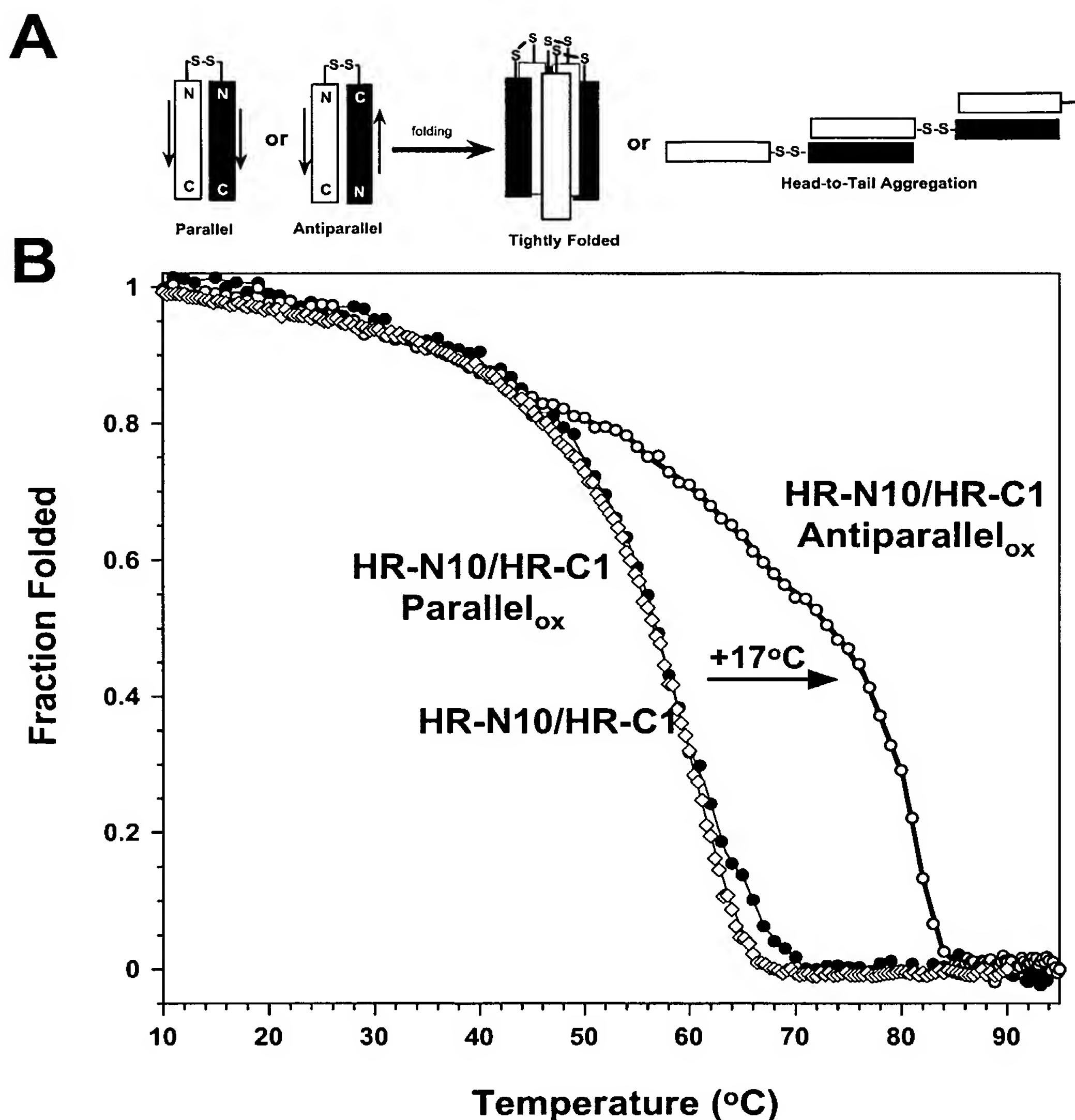


FIG. 9

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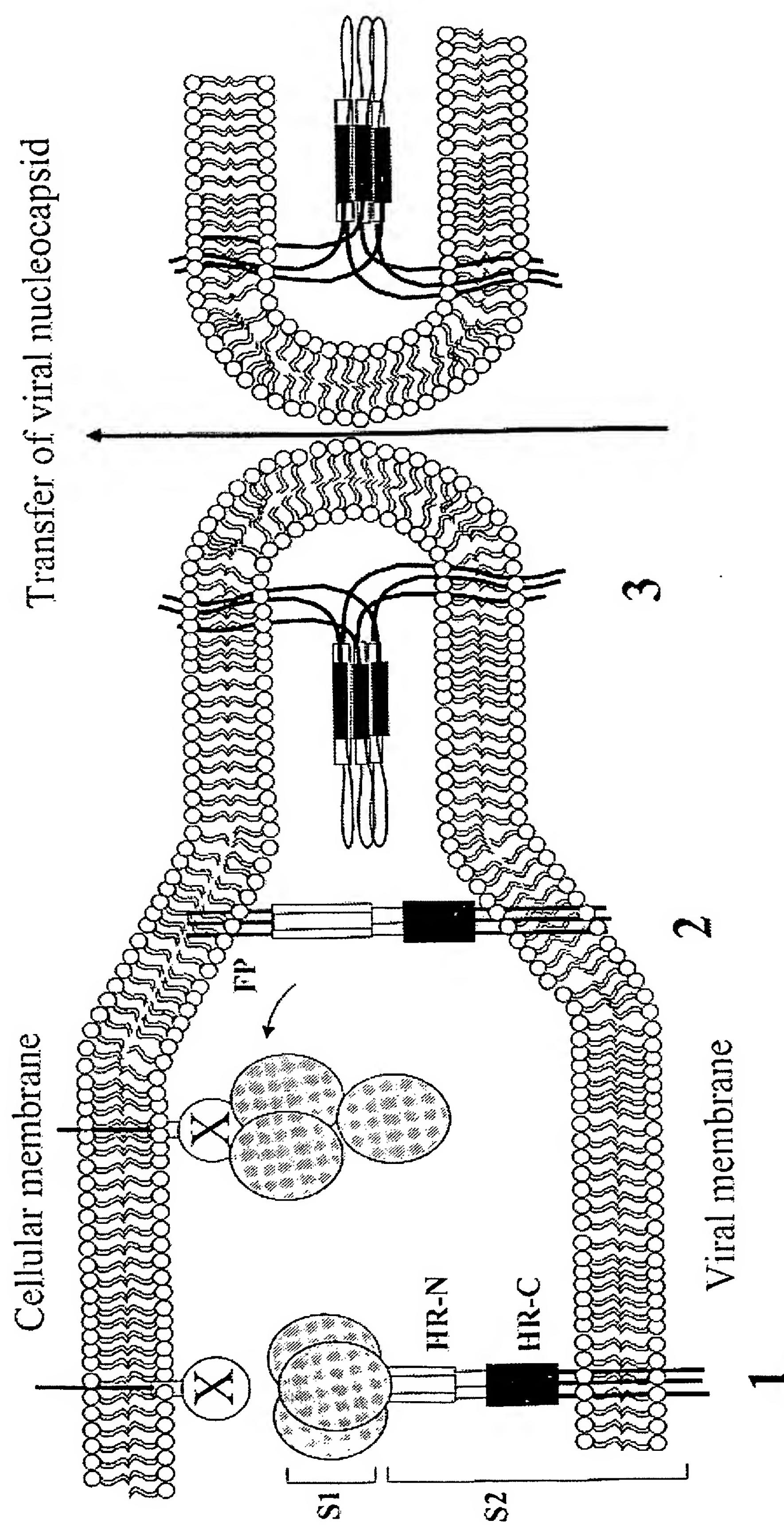


FIG. 10

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## HR-N (916-950)

(native)

Ac-IQESLTTTSTAGKLQDVVNQNAQALNTLVKQLSS-amide

(Ala, Lys and Arg substituted)

Ac-IQAALTKTSAALGKLQAAVNRNAAAALNKLVKALSS-amide

(Aib=B substituted)

Ac-IQESLTBTSTAGKLQDVVNBNAQALNBLVKQLSS-amide

(Dxg=Z substituted)

Ac-IQESLTZTSTAGKLQDVVNZNAQALNZLVKQLSS-amide

## HR-C (1151-1185)

(native)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDDLQEL-amide

(Ala, Lys and Arg substituted)

Ac-IAAINKSVAAIQKEIARLNEVAKALNASLIRLQAL-amide

(Aib=B substituted)

Ac-ISGINBSVVNIQKEIDRLNBVAKNLNBSLIDDLQEL-amide

(Dxg=Z substituted)

Ac-ISGINZSVVNIQKEIDRLNZVAKNLNZSLIDDLQEL-amide

FIG. 11

## HR-N (916-950)

Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

## 1 i,i+4 lactam bridge

Ac-IQESLTTTSTALGKLQEVVNQNAQALNTLVKQLSS-amide  


## 2 i,i+4 lactam bridge

Ac-IQESLTETSTKLGKLQDVVNQNAQALNELVKKLSS-amide  


## 1 i,i+7 bridge

Ac-IQESLTTTSTALGELQDVVNENAQALNTLVKQLSS-amide  


## HR-C (1151-1185)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

## 1 i,i+4 lactam bridge

Ac-ISGINASVVNIQKEIERLNKVAKNLNESLIDLQEL-amide  


## 2 i,i+4 lactam bridge

Ac-ISGINESVVKIQKEIDRLNEVAKNLNESLIKLQEL-amide  


## 1 i,i+7 bridge

Ac-ISGINASVVNIQEEIDRLNEVAKNLNESLIDLQEL-amide  


 = covalent bond

FIG. 12

**HR-N (916-950)**

Ac-IQESLTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

(Ile and Leu substituted into the hydrophobic core)

Ac-IIESLTTITALGKLIDVLNQNIQALNTLIKQLSS-amide

**HR-C (1151-1185)**

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

(Ile substituted into the hydrophobic core)

Ac-ISGINASIVNIQKEIDRLNEVIKNLNESLIDLQEL-amide

**FIG. 13**

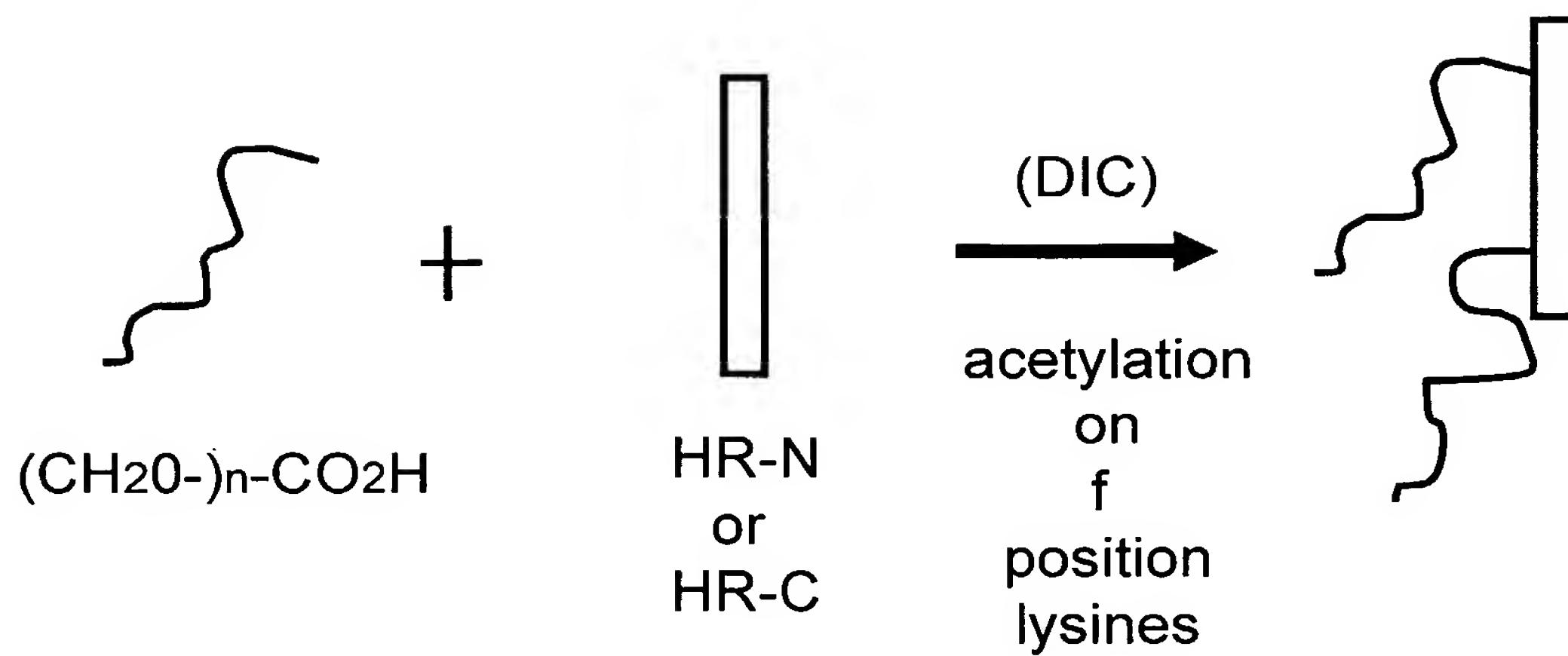


FIG. 14

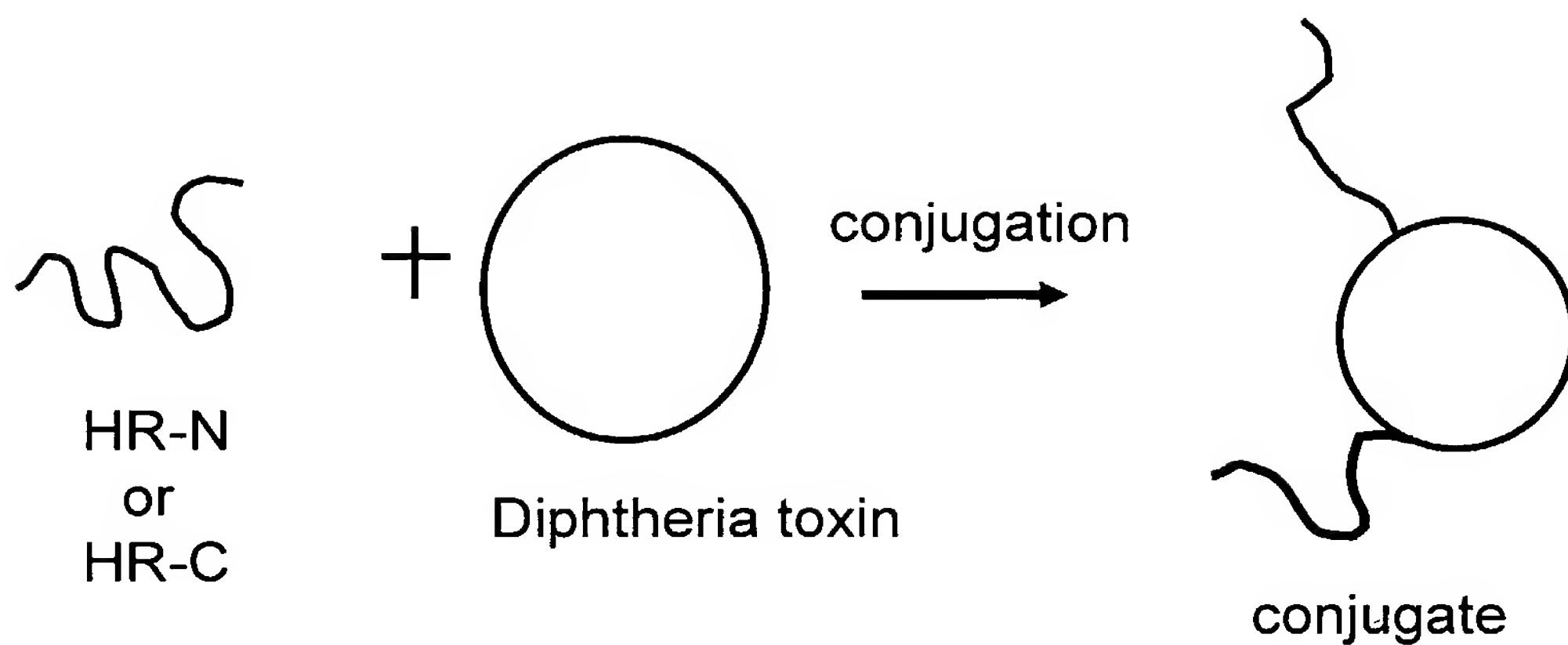


FIG. 15

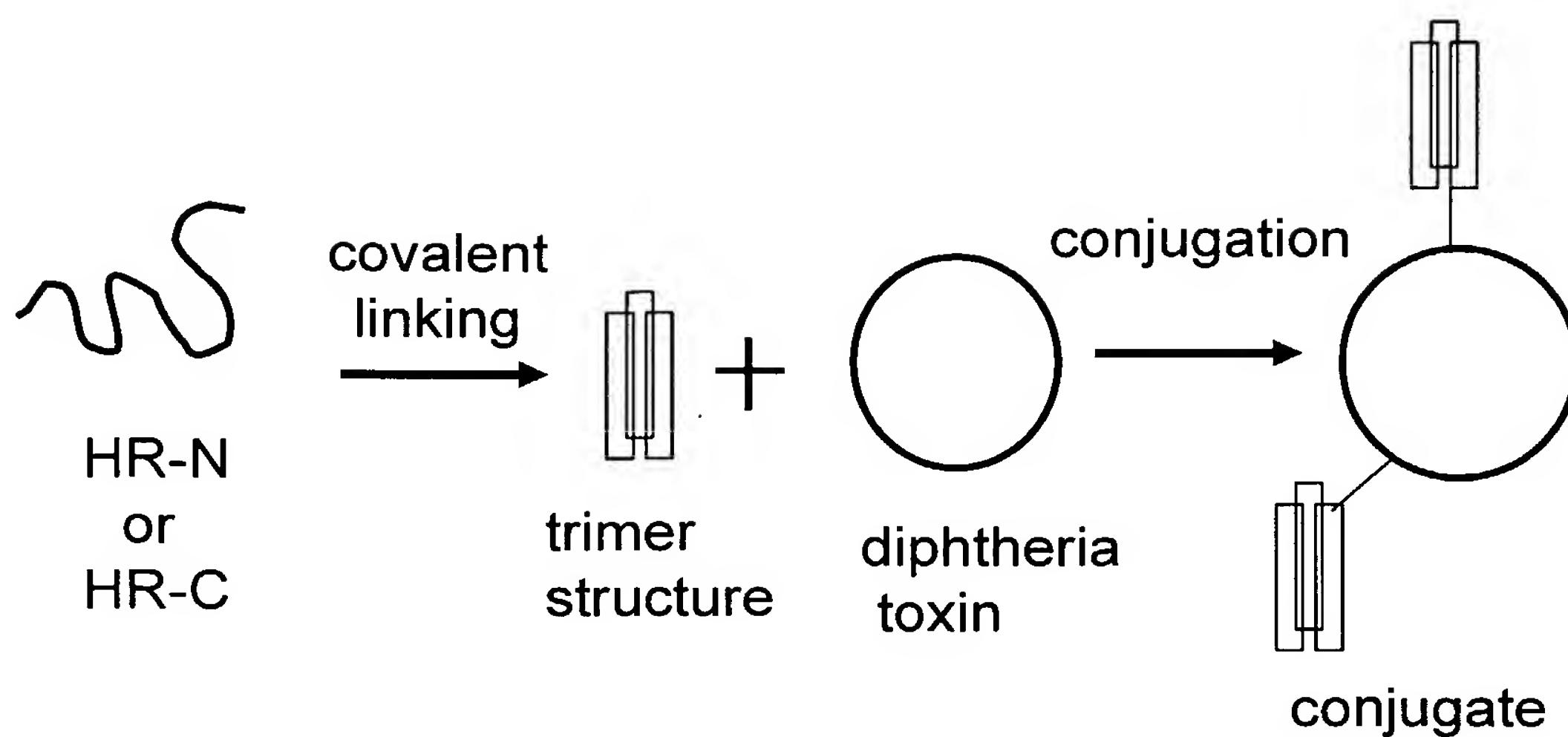


FIG. 16A

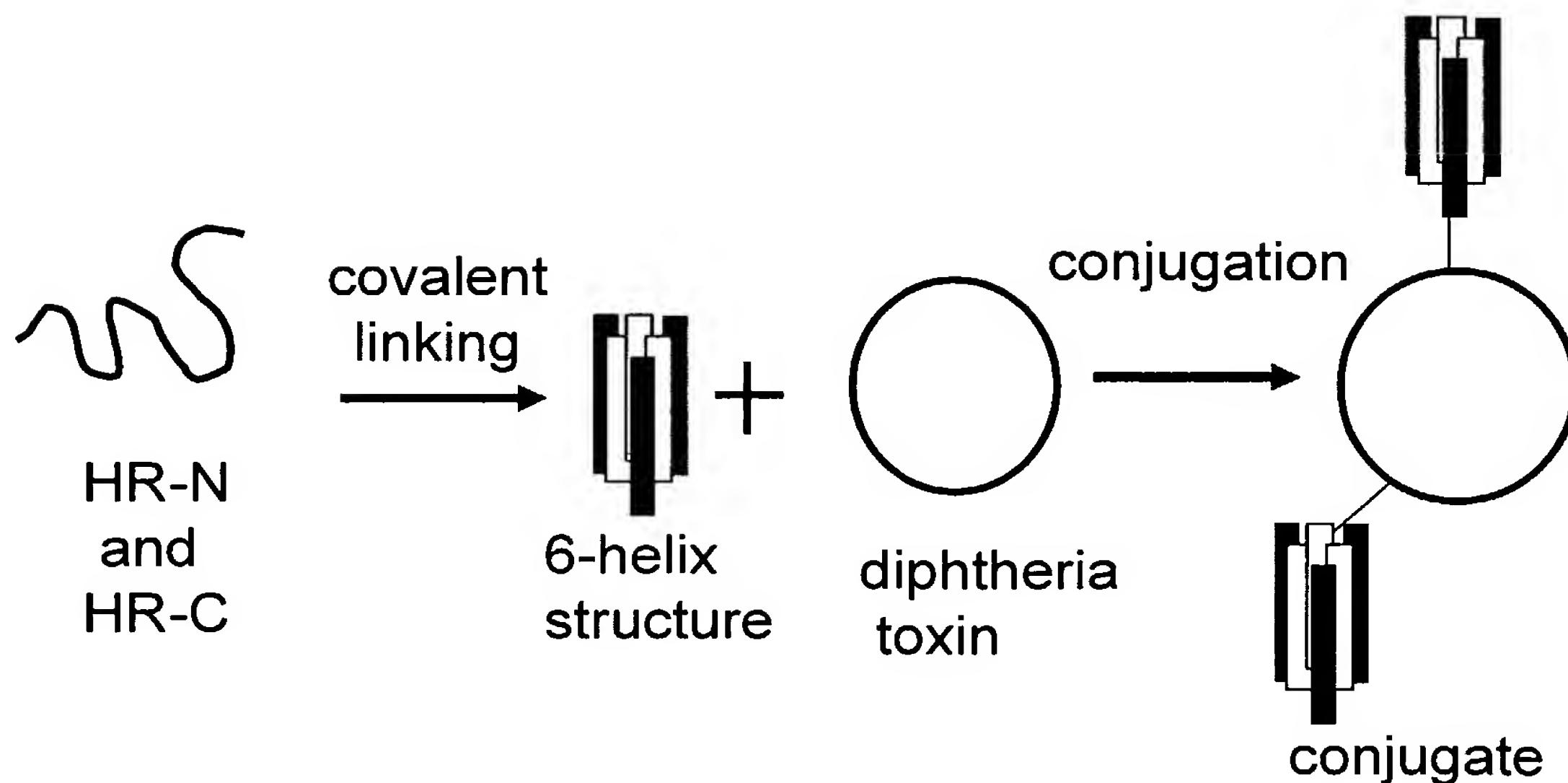


FIG. 16B

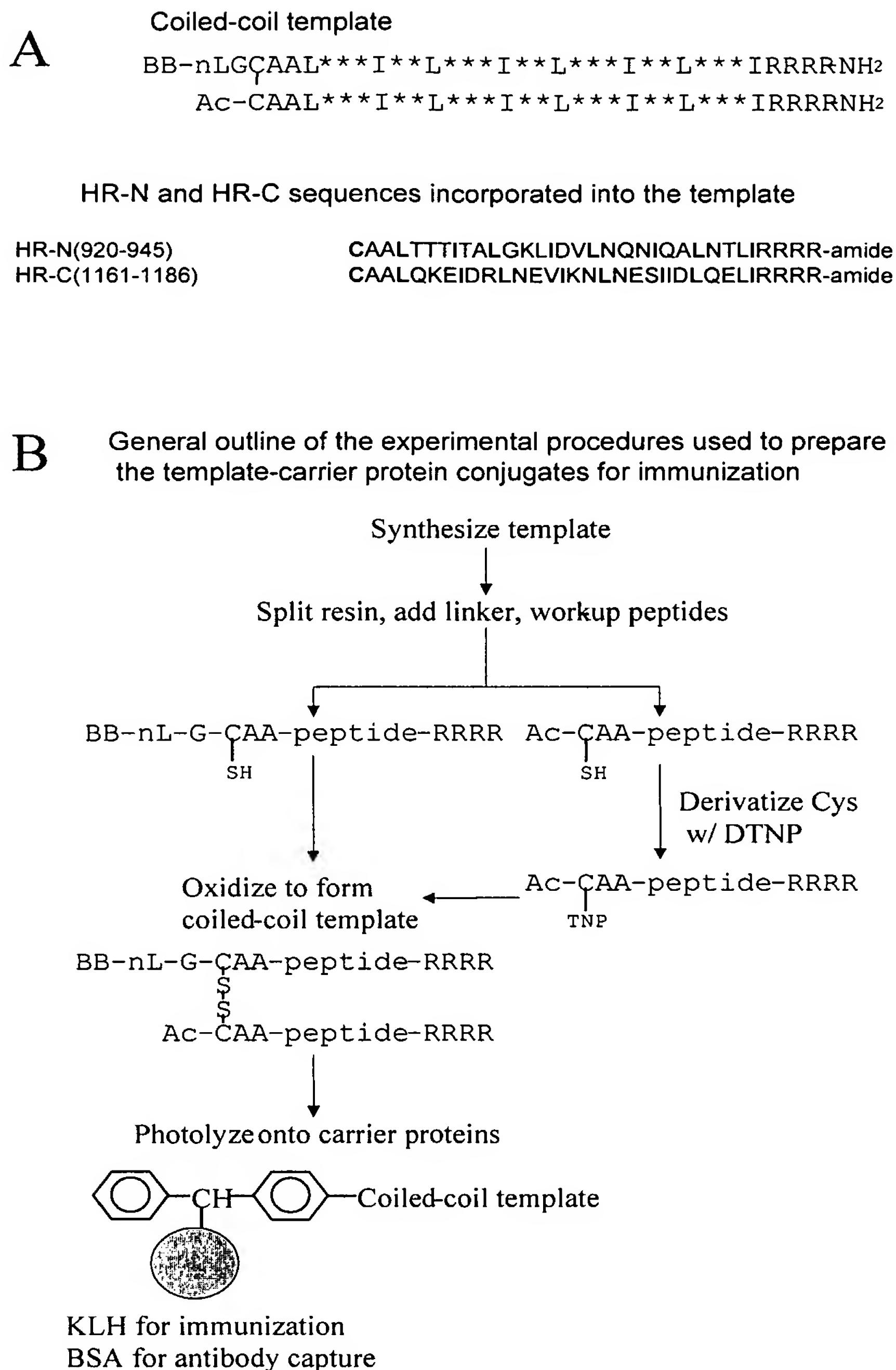


FIG. 17

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HR-N peptides, HR-N1 to HR-N17.

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

**HR-N1 (882-973)**

ATGCAAATGGCATATAGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCA  
AAAACAAATGCCAACCAATTAAACAAGGCGATTAGTCAAATTCAAGAACACTTACAACAA  
CATCAACTGCATTGGCAAGCTGCAAGACGTTAACCAGAACATGCTCAAGCATTAAACACA  
CTTGTAAACAACCTAGCTCAATTGGTGCAATTCAAGTGTGCTAAATGATATCCTTC  
GCGACTTGATAAAGTCGAGGCAGGTA

**HR-N2 (916-973)**

ATTCAAGAACACTTACAACAAACATCAACTGCATTGGCAAGCTGCAAGACGTTAACCA  
GAATGCTCAAGCATTAAACACACTTGTAAACAACTTAGCTCTAATTGGTGCAATTCAA  
GTGTGCTAAATGATATCCTTCGCGACTTGATAAAGTCGAGGCAGGTA

**HR-N3 (927-973)**

TTGGCAAGCTGCAAGACGTTAACCAAGAACATGCTCAAGCATTAAACACACTTGTAAACA  
ACTTAGCTCTAATTGGTGCAATTCAAGTGTGCTAAATGATATCCTTCGCGACTTGATA  
AAGTCGAGGCAGGTA

**HR-N4 (974-1011)**

CAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTCAAACCTATGTAACACAAACACT  
AATCAGGGCTGCTGAAATCAGGGCTCTGCTAATCTGCTGCTACTAAATG

**HR-N5 (882-916)**

ATGCAAATGGCATATAGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCA  
AAAACAAATGCCAACCAATTAAACAAGGCGATTAGTCAAATT

**HR-N6 (888-922)**

TTCAATGGCATGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAACAAATGCCAACCA  
ATTAAACAAGGCGATTAGTCAAATTCAAGAACACTTACAACA

**HR-N7 (895-929)**

CAAAATGTTCTCTATGAGAACCAAAACAAATGCCAACCAATTAAACAAGGCGATTAGTC  
AATTCAAGAACACTTACAACAACATCAACTGCATTGGCAAG

**FIG. 18A**

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**HR-N8 (902-936)**

CAAAAACAAATGCCAACCAATTAAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAAC  
AACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCGAG

**HR-N9 (909-943)**

TTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACAAACATCAACTGCATTGGGCAA  
GCTGCAAGACGTTGTTAACCGAGATGCTCAAGCATTAAACACA

**HR-N10 (916-950)**

ATTCAAGAATCACTTACAACAAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCA  
GAATGCTCAAGCATTAAACACACTTGTAAACAAACTTAGCTCT

**HR-N11 (923-957)**

ACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCGAGATGCTCAAGCATTAAACAC  
ACTTGTAAACAACTTAGCTCTAATTTGGTGCAATTCAAGT

**HR-N12 (931-965)**

CAAGACGTTGTTAACCGAGATGCTCAAGCATTAAACACACTTGTAAACAAACTTAGCTCTAA  
TTTGGTGCAATTCAAGTGTGCTAAATGATATCCTTCGCGA

**HR-N13 (938-972)**

GCTCAAGCATTAAACACACTTGTAAACAACTTAGCTCTAATTTGGTGCAATTCAAGTGT  
GCTAAATGATATCCTTCGCGACTTGATAAAGTCGAGGCAGGAG

**HR-N14 (945-979)**

GTTAAACAACTTAGCTCTAATTTGGTGCAATTCAAGTGTGCTAAATGATATCCTTCGCG  
ACTTGATAAAGTCGAGGCAGGAGGTACAAATTGACAGGTTAATT

**HR-N15 (952-986)**

TTTGGTGCAATTCAAGTGTGCTAAATGATATCCTTCGCGACTTGATAAAGTCGAGGCAGGAG  
GGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTT

**HR-N16 (959-993)**

CTAAATGATATCCTTCGCGACTTGATAAAGTCGAGGCAGGAGGTACAAATTGACAGGTTAAT  
TACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAAACAA

**HR-N17 (966-1000)**

CTTGATAAAGTCGAGGCAGGAGGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCT  
TCAAACCTATGTAACACAAACAACTAATCAGGGCTGCTGAAATC

FIG. 18B

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HR-C peptides, HR-C1 to HR-C4

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

**HR-C1 (1147-1185)**

GATGTTGATCTGGCGACATTCAAGGCATTAACGCTCTGTCGTCAACATTCAAAAAGAAAT  
TGACCGCCTCAATGAGGTCGCTAAAAATTAAATGAATCACTCATTGACCTTCAAGAATTG

**HR-C2 (1165-1185)**

ATTGACCGCCTCAATGAGGTCGCTAAAAATTAAATGAATCACTCATTGACCTTCAAGAATT  
G

**HR-C3 (1158-1185)**

GTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTAAATGAATC  
ACTCATTGACCTTCAAGAATTG

**HR-C4 (1151-1185)**

ATTCAGGCATTAACGCTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGT  
CGCTAAAAATTAAATGAATCACTCATTGACCTTCAAGAATTG

Amino acid sequence for SARS peptide HR-C1

**HR-C1 (1147-1185)**

DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL

FIG. 19

**HR-N**

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

**HR-N (882-1011)**

```
ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAG  
AACCAAAAAACAAATGCCAACCAATTAAACAAGGCATTAGTCAAATTCAAGAATCACTTAC  
AACAAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAA  
ACACACCTGTTAAACAACCTAGCTCTAATTTGGTGCAATTCAAGTGTGCTAAATGATATC  
CTTCGCGACTTGATAAAGTCGAGGCAGGTACAAATTGACAGGTTAATTACAGGCAGACT  
TCAAAGCCTTCAAACCTATGTAACACAACTAATCAGGGCTGCTGAAATCAGGGCTTCTG  
CTAATCTTGCTGCTACTAAAATG
```

**FIG. 20**

ATGTTATTTCTTATTATTCTACTCTCACTAGTGGTAGTGACCTGACCGGTGCACCACTTTGATG  
ATGTTCAAGCTCCTAATTACACTCAACACATACTCATCTATGAGGGGGTTACTATCCTGATGAAATT  
TAGATCAGACACTCTTATTAACTCAGGATTATTCTTCCATTATTCTAATGTTACAGGGTTCAT  
ACTATTAATCATACGTTGGCAACCCTGTACACCTTTAAGGATGGTATTATTGCTGCCACAGAGA  
AATCAAATGTTGCCGGTTGGTTCTACCATGAACAACAAGTCACAGTCGGTATTATT  
TAACAATTCTACTAATGTTGTTACAGAGCATGTAACCTTGAATTGTGTGACAACCCTTCTGCTGTT  
TCTAAACCCATGGGTACACAGACACATACTATGATATTGATAATGCATTAAATTGCACTTCGAGTACA  
TATCTGATGCCTTTCGCTTGATGTTCAGAAAAGTCAGGTAATTAAACACTTACGAGAGTTGTGTT  
AAAAAATAAAGATGGGTTCTCATGTTATAAGGGCTACACCTATAGATGTAGTCGTGATCTACCT  
TCTGGTTTAACACTTGAAACCTATTAAAGTTGCCTTGGTATTAACATTACAAATTAGAGCCA  
TTCTTACAGCCTTTCACCTGCTCAAGACATTGGGCACGTACAGTCAGCCTATTGTTGGCTATT  
AAAGCCAACATACATTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTGATTGTTCTCAA  
AATCCACTTGCTGAACCTAACATGCTGTAAAGAGCTTGAGATTGACAAGGAATTACAGACCTCTA  
ATTTCAGGGTTGTTCCCTCAGGAGATGTTGAGATTCCCTAATATTACAAACTTGTGTCCTTGGAGA  
GGTTTTAATGCTACTAAATTCCCTCTGTCTATGCATGGAGAGAAAAAAATTCTAATTGTTGCT  
GATTACTCTGTGCTCTACAACTCAACATTTCACCTTAAGTGTATGGCTATGGCTTCTGCCACTAAGT  
TGAATGATCTTGCTTCCAATGTCATGCAGATTCTTGTAGTCAGGGAGATGATGTAAGACAAAT  
AGCGCCAGGACAAACTGGTGTATTGCTGATTATAATTAAATTGCCAGATGATTTCATGGGTTGTGTC  
CTGCTTGGAAATACTAGGAACATTGATGCTACTCAACTGGTAATTATAATTAAATATAGGTATCTTA  
GACATGGCAAGCTTAGGCCCTTGAGAGAGACATATCTAATGTGCTTCTCCCCTGATGGCAAACCTG  
CACCCCCACCTGCTCTAATTGTATTGCCATTAAATGATTATGGTTTACACCAACTGGCATTGGC  
TACCAACCTTACAGAGTTGAGACTTCTTTGAACCTTAAATGCACCGGCCACGGTTGACCAA  
AATTATCCACTGACCTTATTAAGAACAGTGTCAATTAAATTAAATGGACTCACTGGTACTGGT  
GTTAACTCCTCTTCAAAGAGATTCAACCATTCAACAATTGGCGTATGTTCTGATTCACTGAT  
TCCGTTGAGATCCTAAACATCTGAAATTAGACATTACCTTGCTCTTGGGGGTGTAAGTGTAA  
TTACACCTGGAACAAATGCTCATCTGAAGTTGCTTCTATATCAAGATGTTACTGCACTGATGTT  
TACAGCAATTCTGCAACTCACACCAGCTGGCGCATATTACTGGAAACATGTATTCCAG  
ACTCAAGCAGGCTGTCTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCACATTCTATTGGAG  
CTGGCATTGCTAGTACCATACAGTTCTTATTACGTAGTACTAGCaaaaATCTATTGTGGCTTA  
TACTATGCTTCTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTA  
TCAATTAGCATTACTACAGAAGTAATGCCCTGTTCTATGGCTAAACCTCCGTAGATTGTAATATGTACA  
TCTGCGGAGATTCTACTGAATGTGCTAATTGCTTCTCCAATATGGTAGCTTGCACACAACAAATCG  
TGCACCTCAGGTATTGCTGCAACAGGATCGAACACACAGTGAAGTGTGCTCAAGTCACAAACAAATG  
TACAAAACCCAACTTGAATATTGGGTTTAATTTCACAAATATTACCTGACCCCTCTAAAGC  
CAACTAAGAGGTCTTTATTGAGGACTTGCTTTAATAAGGTGACACTCGCTGATGCTGGCTCATGAA  
GCAATATGGCAATGCCCTAGGTGATATTAAATGCTAGAGATCTATTGTGCGAGAAGTTCAATGGACTT  
ACAGTGTGCCACCTGCTCACTGATGATATGATTGCTGCCTACACTGCTGCTAGTTAGTGGTACTG  
CCACTGCTGGATGGACATTGGTGTGCTGGCGCTGCTCTCAAATACCTTGTATGCAAATGGCATATAG  
GTTCAATGGCATGGAGTTACCCAAATGTTCTATGAGAACCAAAACAAATGCCAACCAATTAAAC  
AAGGCATTAGTCAAATTCAAGAACACTTACAACACATCAACTGCATTGGCAAGCTGCAAGACGTTG  
TTAACCGAAATGCTCAAGCATTAAACACACTTGTAAACAACATTAGCTCTAATTGGTCAATTCAAG  
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CTAATCTGCTGCTACTAAAATGTCAGTGTGTTCTGGACAATCAAAAGAGTTGACTTTGTGGAAA  
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CCATCCCAGGAGAGGAACCTCACACAGCGCCAGCAATTGTCATGAAGGCAAAGCATACTTCCCTCGTG  
AAGGTGTTTGTGTTAATGGCACTTCTGGTTATTACACAGAGGAACCTCTTTCTCCACAAATAAT  
TACTACAGACAATACATTGCTCAGGAAATTGTGATGTCGTTATTGGCATCTAACACACAGTTAT  
GATCCTCTGCAACCTGAGCTGACTCATCAAAGAAGAGCTGGACAAGTACTCTAAACATACATCAC  
CAGATGTTGATCTGGCGACATTCAAGGCATTAACGCTTCTGTCGTCAACATTCAAAAGAAATTGACCG  
CCTCAATGAGGTGCTAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGAAAATATGAGCAA  
TATATTAAATGGCCTGGTATGTTGGCTGGCTCATTGCTGGACTAATTGCCATGTCATGGTACAA  
TCTTGCTTGTGCACTGACTAGTTGTCAGTTGCCTCAAGGGTGCATGCTCTGTTGCTGCAA  
GTTTGATGAGGATGACTCTGAGCCAGTCTCAAGGGTGTCAAATTACACATAA

FIG. 21

**HR-C Native (SEQ ID NO:48).**

1150	1161	1171	1181
DISGINASVNV	<b>I<u>QKEIDRLNE</u></b>	<b>VAKNLNE</b> SLI	DLQEL
ga d a d	a d	a d a	d

**HR-C Analogue 1 (SEQ ID NO:67). Modulation of the “a” residue position**

1150	1161	1171	1181
DISGINASVNV	<b>I<u>QKEIDRLNE</u></b>	<b>V<u>IKNLNE</u></b> SLI	DLQEL

**HR-C Analogue 2 (SEQ ID NO:68). Change of Helical propensity**

1150	1161	1171	1181
DISGINASVNV	<b>I<u>QKEIARLNE</u></b>	<b>VAKALNE</b> SLI	DLQEL

**HR-C Analogue 3 (SEQ ID NO:69). Change of Helical propensity and modulation of “a” position**

1150	1161	1171	1181
DISGINASVNV	<b>I<u>QKEIARLNE</u></b>	<b>V<u>IKALNE</u></b> SLI	DLQEL

**HR-C Analogue 4 (SEQ ID NO:70). Change of Helical propensity**

1150	1161	1171	1181
DI <u>AA</u> INASV <u>AN</u>	<b>I<u>QKEIARLNE</u></b>	<b>VAKALNE</b> SL <u>A</u>	<u>ALQAL</u>

**HR-C Analogue 5 (SEQ ID NO:71). Introduction of lactam**

1150	1161	1171	1181
DISGINASVNV	<b>I<u>QKEI</u><u>ERLNK</u></b>	<b>VAKNLNE</b> SLI	DLQEL
	[ ]		

**HR-C Analogue 6 (SEQ ID NO:72). Introduction of salt bridge**

1150	1161	1171	1181
DISGINASVNV	<b>I<u>QKEI</u><u>ERLNK</u></b>	<b>VAKNLNE</b> SLI	DLQEL

**HR-C Analogue 7 (SEQ ID NO:73).**

1150	1161	1171	1181
DI <u>EE</u> IN <u>KKV</u> <u>EE</u>	<b>I<u>QK</u><u>KIEELNK</u></b>	<b>KAEELNK</b> <u>KK</u> <u>LE</u>	<u>ELQ</u> <b>KK</b>

**HR-C Analogue 8 (SEQ ID NO:74). Introduction of salt bridges**

1150	1161	1171	1181
DISGINASV <u>VE</u>	<b>I<u>QK</u><u>KKIEELNK</u></b>	<b>KAEELNK</b> <u>KK</u> <u>LI</u>	DLQEL